--Yet another aspect of the present invention is a method for identifying an activator or inhibitor of any molecule or molecular complex which comprises a CoA binding site, including any member of the ACPS-like P-pant transferases, comprising the steps of generating a three dimensional model of said molecule or molecular complex using the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 or Figure 2 and 2A-1 to 2A-19 of residues ARG45, PHE49, ARG53, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104 and HIS105 from one monomer of ACPS, and of ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said residues of not more than 1.5Å, and then selecting or designing a candidate activator or inhibitor that interacts with said molecule or molecular complex using computer fitting analyses of interactions between the three dimensional model of the molecule or molecular complex and the candidate activator or inhibitor. The effect of the candidate activator or inhibitor may be evaluated by obtaining the candidate activator or inhibitor, contacting the same with the molecule or molecular complex, and measuring the effect of the candidate activator or inhibitor on molecular or molecular complex activity.--

Please replace the paragraph on page 5, line 26 through page 6, line 11, with the following:

--Alternatively, the three dimensional model of the molecule or molecular complex comprising a CoA binding site may be determined using the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 or Figure 2 and 2A-1 to 2A-19 of residues ARG53, ASN84, GLY85, LYS86, PRO87, ILE103, THR104, and HIS105 from one monomer of ACPS and ASP8, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, or alternatively, of residues LEU41, ARG45, GLU48, PHE49, LEU50, ALA51, GLY52, ILE79,

ARG80, LYS81, ASP82, GLN83, TYR88, VAL101, SER102, THR106, TYR109, ALA110, and ALA111 from one monomer of ACPS and ILE5, GLY6, LEU7, ILE9, THR10, ARG14, ILE15, MET18, GLN22, ALA55, LYS57, ALA59, PHE60, ALA63, PHE64, GLY69, ARG70, GLN71 and LEU72 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å. Also provided by the present invention are the activators or inhibitors selected or designed using the above-noted methods.--

Please replace the paragraph on page 6, line 22 through page 7, line 14, with the following:

--Finally, the present invention provides the CoA active site of an ACPS-like P-pant transferase, including, but not limited to, an ACPS, comprising, alternatively, (a) the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 of ARG45, PHE49, ARG53, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104 and HIS105 from one monomer of ACPS, and ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, (b) the structural coordinates according to Figure 1 and 1A-1 to 1A-107 of residues ARG53, ASN84, GLY85, LYS86, PRO87, ILE103, THR104, and HIS105 from one monomer of ACPS and ASP8, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or (c) the structural coordinates according to Figure 1 and 1A-1 to 1A-107 of residues LEU41, ARG45, GLU48, PHE49, LEU50, ALA51, GLY52, ILE79, ARG80, LYS81, ASP82, GLN83, TYR88, VAL101, SER102, THR106, TYR109, ALA110, and ALA111 from one monomer of ACPS and ILE5, GLY6, LEU7, ILE9, THR10, ARG14, ILE15, MET18, GLN22, ALA55, LYS57,

ALA59, PHE60, ALA63, PHE64, GLY69, ARG70, GLN71 and LEU72 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.--

Please replace the paragraph on page 7, line 15 through page 8, line 8, with the following:

--In an additional embodiment, the present invention provides the CoA active site of an ACPS-like P-pant transferase, including, but not limited to, an ACPS, wherein said active site is in its bound configuration, and comprising alternatively, (a) the relative structural coordinates according to Figure 2 and 2A-1 to 2A-19 of ARG45, PHE49, ARG53, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104 and HIS105 from one monomer of ACPS, and ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, (b) the structural coordinates according to Figure 2 and 2A-1 to 2A-19 of residues ARG53, ASN84, GLY85, LYS86, PRO87, ILE103, THR104, and HIS105 from one monomer of ACPS and ASP8, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or (c) the structural coordinates according to Figure 2 and 2A-1 to 2A-19 of residues LEU41, ARG45, GLU48, PHE49, LEU50, ALA51, GLY52, ILE79, ARG80, LYS81, ASP82, GLN83, TYR88, VAL101, SER102, THR106, TYR109, ALA110, and ALA111 from one monomer of ACPS and ILE5, GLY6, LEU7, ILE9, THR10, ARG14, ILE15, MET18, GLN22, ALA55, LYS57, ALA59, PHE60, ALA63, PHE64, GLY69, ARG70, GLN71 and LEU72 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.--

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Please replace the paragraph on page 8, lines 11-19, with the following:

--Figure 1 and 1A-1 to 1A-107 lists the atomic structure coordinates for ACPS as derived by X-ray diffraction of an ACPS crystal. "Atom type" refers to the atom whose coordinates are being measured. "Residue" refers to the type of residue of which each measured atom is a part - i.e., amino acid, cofactor, ligand or solvent. The "x, y and z" coordinates indicate the Cartesian coordinates of each measured atom's location in the unit cell (Å). "Occ" indicates the occupancy factor. "B" indicates the "B-value", which is a measure of how mobile the atom is in the atomic structure (Å^2). "MOL" indicates the segment identification used to uniquely identify each molecule.--

Please replace the paragraph on page 8, lines 20-22, with the following:

--Figure 2 and 2A-1 to 2A-19 lists the atomic structure coordinates for ACPS and CoA as derived by X-ray diffraction of an ACPS-CoA crystal. Figure headings are as noted above.--

Please replace the paragraph on page 10, line 23 through page 11, line 10, with the following:

--As used herein, the protein used in the ACPS crystals and crystal complexes of the present invention includes any protein (i.e., as used herein, any protein, polypeptide or peptide), isolated from any source (including, but not limited to, a protein isolated from *Aquifex*, *Chlamydophila*, *Helicobacter*, *Staphylococcus*, *Thermotoga*, *Escherichia*, *Rickettsia*, *Streptomyces*, *Treponema*, *Bacillus*, *Bradyrhizobium*, and *Mycobacterium*), wherein said protein has ACPS-like P-pant transferase activity, and further comprises the consensus sequence as shown in Figure 9. Additionally, the protein used in the ACPS crystals and crystal complexes of the present invention includes proteins having ACPS-like P-pant transferase activity which comprise the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 or Figure 2 and 2A-1 to 2A-19 for the residues

GLY6, ASP8, ALA51, LYS57, GLU58, ARG53, ALA59, LYS62 and ALA63, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably not more than 1.0Å, or most preferably, not more than 0.5Å. In a preferred embodiment of the invention and as exemplified below, ACPS is cloned and isolated from *B. subtilis*, and then overexpressed in a commercially available *E. coli* system.--

Please replace the paragraph on page 11, lines 11-25, with the following:

--In an alternate embodiment of the present invention, the ACPS used to generate the crystals and/or crystal complexes of the present invention comprises amino acid residues ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, ARG45, PHE49, ARG53, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68, PHE74, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104, and HIS105, or conservative substitutions thereof. These amino acids constitute a depression which defines the CoA active site in the three dimensional structure of the ACPS enzyme, wherein the depression is more particularly comprised of the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 or Figure 2 and 2A-1 to 2A-19 of residues ARG45, PHE49, ARG53, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104 and HIS105 from one monomer of ACPS, and residues ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second molecule of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably not more than 1.0Å, or most preferably, not more than 0.5Å.--

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Please replace the paragraph on page 11, line 26 through page 12, line 8, with the following:

--There are six ACPS molecules in the asymmetric unit of the ACPS crystal. In one embodiment of the invention, the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 of the two monomers forming the depression defining the CoA active site are of residues ARG45, PHE49, ARG53, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104 and HIS105 from ACPS1, and residues ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from ACPS2. In alternate embodiments, the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 are from ACPS2 and ACPS3, respectively; from ACPS1 and ACPS3, respectively; from ACPS4 and ACPS5, respectively; from ACPS5 and ACPS6, respectively; and from ACPS4 and ACPS6, respectively.--

Please replace the paragraph on page 12, lines 9-26, with the following:

--In an alternate preferred embodiment, the ACPS used to generate the crystals and/or crystal complexes of the present invention comprises amino acid residues which are within 4Å of the CoA molecule associated with the ACPS CoA binding site. In a specific embodiment, the ACPS comprises amino acid residues ASP8, PHE25, ARG28, ILE29, ARG53, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68, PHE74, ASN84, GLY85, LYS86, PRO87, ILE103, THR104, and HIS105, or conservative substitutions thereof. Such residues specifically comprise the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 or Figure 2 and 2A-1 to 2A-19 of residues ARG53, ASN84, GLY85, LYS86, PRO87, ILE103, THR104, and HIS105 from one monomer of ACPS and ASP8, PHE25, ARG28, ILE29, PHE24, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68, and PHE74 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably not more than 1.0Å, or most preferably, not more than 0.5Å. In alternate embodiments, the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 are from ACPS1 and ACPS2, respectively; from ACPS2 and ACPS3,

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respectively; from ACPS1 and ACPS3, respectively; from ACPS4 and ACPS5, respectively; from ACPS5 and ACPS6, respectively; and from ACPS4 and ACPS6, respectively.--

Please replace the paragraph on page 12, line 27 through page 13, line 20, with the following:

--In yet another alternate preferred embodiment, the ACPS used to generate the crystals and/or crystal complexes of the present invention comprises amino acid residues which are within 4Å to 8Å of the CoA molecule associated with the ACPS CoA binding site. Specifically, such residues include ILE5, GLY6, LEU7, ILE9, THR10, ARG14, ILE15, MET18, GLN22, LEU41, ARG45, GLU48, PHE49, LEU50, ALA51, GLY52, ALA55, LYS57, ALA59, PHE60, ALA63, PHE64, GLY69, ARG70, GLN71, LEU72, ILE79, ARG80, LYS81, ASP82, GLN83, TYR88, VAL101, SER102, THR106, TYR109, ALA110, and ALA111, or conservative substitutions thereof. Such residues more particularly comprise the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 or Figure 2 and 2A-1 to 2A-19 of residues LEU41, ARG45, GLU48, PHE49, LEU50, ALA51, GLY52, ILE79, ARG80, LYS81, ASP82, GLN83, TYR88, VAL101, SER102, THR106, TYR109, ALA110, and ALA111 from one monomer of ACPS and ILE5, GLY6, LEU7, ILE9, THR10, ARG14, ILE15, MET18, GLN22, ALA55, LYS57, ALA59, PHE60, ALA63, PHE64, GLY69, ARG70, GLN71 and LEU72 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å (or more preferably not more than 1.0Å, or most preferably, not more than 0.5Å), and more specifically may comprise the relative structural coordinates of residues according to Figure 1 and 1A-1 to 1A-107 from ACPS1 and ACPS2, respectively; from ACPS2 and ACPS3, respectively; from ACPS1 and ACPS3, respectively; from ACPS4 and ACPS5, respectively; from ACPS5 and ACPS6, respectively; and from ACPS4 and ACPS6, respectively.--

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Please replace the paragraph on page 13, lines 21-26, with the following:

--Further, the ACPS used to generate the crystals and/or crystal complexes of the present invention may comprise the entire 121 amino acid residues of Figure 8, and the structural coordinates of these residues according to Figure 1 and 1A-1 to 1A-107 or Figure 2 and 2A-1 to 2A-19, ± a root mean square deviation from the backbone atoms of said amino acid residues of not more than 1.5Å, or more preferably not more than 1.0Å, or most preferably, not more than 0.5Å.--

Please replace the paragraph on page 15, lines 10-28, with the following:

--As used herein, an "active site" refers to a region of a molecule or molecular complex that, as a result of its shape and charge potential, interacts with another agent (including, without limitation, a protein, polypeptide, peptide, nucleic acid, including DNA or RNA, molecule, compound, antibiotic or drug). The agent may be an activator or inhibitor of the molecular or molecular complex activity. The present invention is directed to a CoA active site of an ACPS-like P-pant transferase, including the active site of an acyl carrier protein synthase, comprising the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 of residues ARG45, PHE49, ARG53, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104 and HIS105 from one monomer of ACPS, and of ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably not more than 1.0Å, or most preferably, not more than 0.5Å. More specifically, the active site of ACPS in its native (i.e., unbound) state may comprise the relative structural coordinates of the residues according to Figure 1 and 1A-1 to 1A-107 from ACPS1 and ACPS2, respectively; from ACPS2 and ACPS3, respectively; from ACPS1 and ACPS3, respectively; from ACPS4 and

ACPS5, respectively; from ACPS5 and ACPS6, respectively; and from ACPS4 and ACPS6, respectively.---

Please replace the paragraph on page 16, lines 1-12, with the following:

--In an alternate embodiment, the CoA active site of the present invention comprises the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 of residues ARG53, ASN84, GLY85, LYS86, PRO87, ILE103, THR104, and HIS105 from one monomer of ACPS and of residues ASP8, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably not more than 1.0Å, or most preferably, not more than 0.5Å. The active site may comprise the relative structural coordinates of the residues according to Figure 1 and 1A-1 to 1A-107 from ACPS1 and ACPS2, respectively; from ACPS2 and ACPS3, respectively; from ACPS1 and ACPS3, respectively; from ACPS4 and ACPS5, respectively; from ACPS5 and ACPS6, respectively; and from ACPS4 and ACPS6, respectively.---

Please replace the paragraph on page 16, lines 13-26, with the following:

--In a yet further embodiment, the CoA active site of the present invention comprises the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 of residues LEU41, ARG45, GLU48, PHE49, LEU50, ALA51, GLY52, ILE79, ARG80, LYS81, ASP82, GLN83, TYR88, VAL101, SER102, THR106, TYR109, ALA110, and ALA111 from one monomer of ACPS and of residues ILE5, GLY6, LEU7, ILE9, THR10, ARG14, ILE15, MET18, GLN22, ALA55, LYS57, ALA59, PHE60, ALA63, PHE64, GLY69, ARG70, GLN71 and LEU72 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably, not more than 1.0Å, and most preferably, not more than 0.5Å. The active

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site may comprise the relative structural coordinates of the residues according to Figure 1 and 1A-1 to 1A-107 from ACPS1 and ACPS2, respectively; from ACPS2 and ACPS3, respectively; from ACPS1 and ACPS3, respectively; from ACPS4 and ACPS5, respectively; from ACPS5 and ACPS6, respectively; and from ACPS4 and ACPS6, respectively.--

Please replace the paragraph on page 16, line 27 through page 17, line 4, with the following:

--Further still, an alternate embodiment of the CoA active site of the present invention comprises the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 of GLY6, ASP8, ALA51, ARG53, LYS57, GLU58, ALA59, LYS62 and ALA63, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably, not more than 1.0Å, and most preferably, not more than 0.5Å.--

Please replace the paragraph on page 17, lines 12-20, with the following:

--In a preferred embodiment of the invention, the CoA active site in its bound state comprises the relative structural coordinates according to Figure 2 and 2A-1 to 2A-19 of residues ARG45, PHE49, ARG53, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104 and HIS105 from one monomer of ACPS, and of ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably not more than 1.0Å, or most preferably, not more than 0.5Å.--

Please replace the paragraph on page 17, lines 21-28, with the following:

--In an alternate embodiment, the active site comprises the relative structural coordinates according to Figure 2 and 2A-1 to 2A-19 of residues ARG53, ASN84, GLY85,

LYS86, PRO87, ILE103, THR104, and HIS105 from one monomer of ACPS and of residues ASP8, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably not more than 1.0Å, or most preferably, not more than 0.5Å.--

Please replace the paragraph on page 18, lines 1-9, with the following:

--In a yet further embodiment, the active site comprises the relative structural coordinates according to Figure 2 and 2A-1 to 2A-19 of residues LEU41, ARG45, GLU48, PHE49, LEU50, ALA51, GLY52, ILE79, ARG80, LYS81, ASP82, GLN83, TYR88, VAL101, SER102, THR106, TYR109, ALA110, and ALA111 from one monomer of ACPS and of residues ILE5, GLY6, LEU7, ILE9, THR10, ARG14, ILE15, MET18, GLN22, ALA55, LYS57, ALA59, PHE60, ALA63, PHE64, GLY69, ARG70, GLN71 and LEU72 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably, not more than 1.0Å, and most preferably, not more than 0.5Å.--

Please replace the paragraph on page 18, lines 10-14, with the following:

--Finally, a CoA active site of the present invention comprises the relative structural coordinates according to Figure 2 and 2A-1 to 2A-19 of GLY6, ASP8, ALA51, ARG53, LYS57, GLU58, ALA59, LYS62 and ALA63, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably, not more than 1.0Å, and most preferably, not more than 0.5Å.--

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Please replace the paragraph on page 20, line 13 through page 21, line 6, with the following:

--The present invention is not limited to identifying agents which interact with an active site of ACPS or ACPS-CoA complex, but also is directed to a method for identifying an activator or inhibitor of any molecule or molecular complex comprising a CoA binding site, comprising the first step of generating a three dimensional model of said molecule or molecular complex comprising a CoA binding site using the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 or Figure 2 and 2A-1 to 2A-19 of residues ARG45, PHE49, ARG53, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104 and HIS105 from one monomer of ACPS, and of ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably not more than 1.0Å, or most preferably, not more than 0.5Å. In alternate embodiments, the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 are from ACPS1 and ACPS2, respectively; from ACPS2 and ACPS3, respectively; from ACPS1 and ACPS3, respectively; from ACPS4 and ACPS5, respectively; from ACPS5 and ACPS6, respectively; and from ACPS4 and ACPS6, respectively. Then, a candidate activator or inhibitor is selected or designed by performing computer fitting analyses of said candidate agent with the three dimensional model of the molecule or molecular complex comprising a CoA active site. Once the candidate activator or inhibitor is obtained, it may be contacted with the molecule or molecular complex in order to measure the effect the candidate activator or inhibitor has on said molecule or molecular complex.--

Please replace the paragraph on page 21, lines 7-24, with the following:

--Alternatively, the three dimensional structure of the molecule or molecular complex comprising a CoA binding site may be determined using (a) the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 or Figure 2 and 2A-1 to

2A-19 of residues ARG53, ASN84, GLY85, LYS86, PRO87, ILE103, THR104, and HIS105 from one monomer of ACPS and of residues ASP8, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, or (b) of LEU41, ARG45, GLU48, PHE49, LEU50, ALA51, GLY52, ILE79, ARG80, LYS81, ASP82, GLN83, TYR88, VAL101, SER102, THR106, TYR109, ALA110, and ALA111 from one monomer of ACPS and of residues ILE5, GLY6, LEU7, ILE9, THR10, ARG14, ILE15, MET18, GLN22, ALA55, LYS57, ALA59, PHE60, ALA63, PHE64, GLY69, ARG70, GLN71 and LEU72 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably not more than 1.0Å, or most preferably, not more than 0.5Å. Again, in alternate embodiments, the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 are from ACPS1 and ACPS2, respectively; from ACPS2 and ACPS3, respectively; from ACPS1 and ACPS3, respectively; from ACPS4 and ACPS5, respectively; from ACPS5 and ACPS6, respectively; and from ACPS4 and ACPS6, respectively.---

B7 Cancel

In the Claims:

Please cancel claims 1-14 and 23-34 without disclaimer or prejudice to applicants' right to pursue the subject matter of these claims in a future continuation or divisional application.

Please amend claims 15 and 19 as follows:

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--15. (Amended) A method for identifying an agent that interacts with an active site of acyl carrier protein synthase (ACPS), comprising the steps of: